WHAT IS CLAIMED IS:

1. A set of nucleic acids comprising:
a first nucleic acid containing SEQ ID NO:1 or 3, and
a second nucleic acid containing SEQ ID NO:2 or 4,
wherein each nucleic acid is 18-40 nucleotides in length.

2. The set of nucleic acids of claim 1, wherein the first nucleic acid contains SEQ ID NO:1 and the second nucleic acid contains SEQ ID NO:2.

3. The set of nucleic acids of claim 2, wherein each nucleic acid is 18-30 nucleotides in length.

4. The set of nucleic acids of claim 3, wherein the first nucleic acid is SEQ ID NO:1 and the second nucleic acid is SEQ ID NO:2.

5. The set of nucleic acids of claim 1, wherein the first nucleic acid contains SEQ ID NO:3 and the second nucleic acid contains SEQ ID NO:4.

6. The set of nucleic acids of claim 5, wherein each nucleic acid is 24-32 nucleotides in length.

7. The set of nucleic acids of claim 6, wherein the first nucleic acid is SEQ ID NO:3 and the second nucleic acid is SEQ ID NO:4.

8. A nucleic acid obtained from amplification of an *Escherichia coli* nucleic acid template with an upstream primer containing SEQ ID NO:1 or 3 and a downstream primer containing SEQ ID NO:2 or 4, wherein each primer is 18-40 nucleotides in length.

9. The nucleic acid of claim 8, wherein the upstream primer contains SEQ ID NO:1 and the downstream primer contains SEQ ID NO:2.

10. The nucleic acid of claim 9, wherein each primer is 18-30 nucleotides in length.

11. The nucleic acid of claim 10, wherein the upstream primer is SEQ ID NO:1 and the downstream primer is SEQ ID NO:2.

12. The nucleic acid of claim 8, wherein the upstream primer contains SEQ ID NO:3 and the downstream primer contains SEQ ID NO:4.

13. The nucleic acid of claim 12, wherein each primer is 24-32 nucleotides in length.

14. The nucleic acid of claim 13, wherein the upstream primer is SEQ ID NO:3 and the downstream primer is SEQ ID NO:4.

15. A nucleic acid that is 26-1000 nucleotides in length comprising a sequence selected from the group consisting of SEQ ID NOs:5-8, or a sequence complementary thereto.

16. The nucleic acid of claim 15, wherein said nucleic acid is 26-500 nucleotides in length.

17. The nucleic acid of claim 16, wherein said nucleic acid is 26-200 nucleotides in length.

18. The nucleic acid of claim 17, wherein said nucleic acid is 26-50 nucleotides in length.

19. The nucleic acid of claim 18, wherein said nucleic acid is SEQ ID NO:5.

20. The nucleic acid of claim 18, wherein said nucleic acid is SEQ ID NO:6.

21. The nucleic acid of claim 18, wherein said nucleic acid is SEQ ID NO:7.

22. The nucleic acid of claim 18, wherein said nucleic acid is SEQ ID NO:8.

23. The nucleic acid of claim 15, wherein said nucleic acid is SEQ ID NO:5.

24. The nucleic acid of claim 15, wherein said nucleic acid is SEQ ID NO:6.

25. The nucleic acid of claim 15, wherein said nucleic acid is SEQ ID NO:7.

26. The nucleic acid of claim 15, wherein said nucleic acid is SEQ ID NO:8.

27. A method of detecting *Escherichia coli*, comprising:

providing a sample having a nucleic acid from an unknown microorganism;

amplifying the nucleic acid with an upstream primer containing SEQ ID NO:1 or 3 and a downstream primer containing SEQ ID NO:2 or 4, each primer being 18-40 nucleotides in length; and

detecting an amplification product;

whereby detection of the amplification product indicates the presence of *Escherichia coli*.

28. The method of claim 27, wherein the upstream primer contains SEQ ID NO:1 and the downstream primer contains SEQ ID NO:2.

29. The method of claim 28, wherein each primer is 18-30 nucleotides in length.

30. The method of claim 29, wherein the detecting step includes hybridizing the amplification product to a nucleic acid probe that is 26-1000 nucleotides in length and contains a sequence selected from the group consisting of SEQ ID NOs:5-8, or a sequence complementary thereto.

31. The method of claim 30, wherein said nucleic acid probe is 26-50 nucleotides in length.

32. The method of claim 27, wherein the upstream primer contains SEQ ID NO:3 and the downstream primer contains SEQ ID NO:4.

33. The method of claim 32, wherein each primer is 24-32 nucleotides in length.

34. The method of claim 33, wherein the detecting step includes hybridizing the amplification product to a nucleic acid probe that is 26-1000 nucleotides in length and contains a sequence selected from the group consisting of SEQ ID NOs:5-8, or a sequence complementary thereto.

35. The method of claim 34, wherein said nucleic acid probe is 26-50 nucleotides in length.